

AMENDMENTS TO THE CLAIMS:

The following listing of claims replaces all prior versions and listings in the application:

Listing of Claims:

1. (Currently amended) A method of associative analysis, comprising:

- collecting a plurality of expression profiles of a control group and a plurality of expression profiles of an experimental group;
- normalizing the plurality of expression profiles of the control group relative to their backgrounds;
- normalizing the plurality of expression profiles of the experimental group relative to their backgrounds;
- adjusting the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group, the adjusting comprising:
 - identifying outliers in the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group; and
 - re-scaling the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group to an averaged profile of the control group to diminish or exclude influence of the identified outliers;
- identifying a group of similarly expressed genes, defining a reference group, determined from the plurality of expression profiles of the control group;
- identifying a plurality of differentially expressed genes in the plurality of expression profiles of the experimental group based on the reference group, wherein identifying the plurality of differentially expressed genes comprises utilizing a paired T-test and an associative T-test, the associative T-test comprising a [[test]] T-test in which a plurality of replicated residuals for each gene of the plurality of the expression profiles of the experimental group are compared with an entire set of residuals from the plurality of expression profiles of the control group; and

determining a classification of the differentially expressed genes as (a) likely false positive, (b) real positives, or (c) potential positives using the paired T-test and associative T-test, wherein determining the classification comprises:

classifying the genes identified as expressed by the paired T-test and not identified as expressed by the associative T-test as likely false positives;

classifying the genes identified as expressed by the paired T-test and the associative T-test as real positives; and

classifying the genes identified as expressed by the associative T-test and not identified as expressed by the paired T-test as potential positives; and

outputting the classified real positives to a user.

2. (Canceled)

3. (Previously Presented) The method of claim 1, wherein adjusting the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group further comprises:

selecting a plurality of genes from the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group, wherein the plurality of genes are expressed above a background; and

scaling the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group to an average profile of the plurality of expression profiles of the control group.

4. (Previously Presented) The method of claim 1, wherein adjusting the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group further comprises analyzing by regression analysis the plurality of genes expressed above the background.

5. (Previously Presented) The method of claim 1, wherein adjusting the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group further comprises selecting equally expressed genes as a homogenous family of genes with normally distributed residuals measured as deviations from a regression line that is calculated against an average profile.

6. (Original) The method of claim 1, wherein the reference group comprises a group of genes expressed above background levels with normal low variability of expression in control samples as determined by a F-test.

7. (Original) The method of claim 1, wherein the reference group has residuals that approximate a normal distribution, based on a Kolmogorov-Smirnov criterion.

8. (Canceled)

9. (Original) The method of claim 1, wherein the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group comprise an array.

10. (Canceled)

11. (Previously Presented) The method of claim 1, wherein the genes identified as expressed by the associative T-test are tested again.

12. (Original) The method of claim 1, wherein identifying a group of similarly expressed genes determined from the plurality of expression profiles of the control group further comprises excluding outliers from the plurality of expression profiles of the control group.

13. (Currently amended) A method of associative analysis, comprising:

- collecting a plurality of expression profiles of a control group and a plurality of expression profiles of an experimental group;
- normalizing the plurality of expression profiles of the control group relative to their backgrounds;
- normalizing the plurality of expression profiles of the experimental group relative to their backgrounds;
- adjusting the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group, the adjusting comprising:
 - identifying outliers in the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group; and
 - re-scaling the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group to an averaged profile of the control group to diminish or exclude influence of the identified outliers;
- identifying a group of similarly expressed genes, defining a reference group, determined from the plurality of expression profiles of the control group, the reference group comprising a group of genes expressed above background levels with normal low variability of expression in control samples as determined by a F-test;
- identifying a plurality of differentially expressed genes in the plurality of expression profiles of the experimental group based on the reference group, wherein identifying the plurality of differentially expressed genes comprises utilizing a paired T-test and an associative T-test,
 - wherein the associative T-test comprises a [[test]] T-test in which a plurality of replicated residuals for each gene of the plurality of the expression profiles of the experimental group are compared with an entire set of residuals from the plurality of expression profiles of the control group;

determining a classification of the differentially expressed genes as (a) likely false positive, (b) real positives, or (c) potential positives using the paired T-test and associative T-test, wherein determining the classification comprises:

classifying the genes identified as expressed by the paired T-test and not identified as expressed by the associative T-test as likely false positives;

classifying the genes identified as expressed by the paired T-test and the associative T-test as real positives; and

classifying the genes identified as expressed by the associative T-test and not identified as expressed by the paired T-test as potential positives; and

outputting the classified real positives to a user.